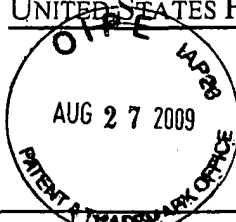




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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/511,130

08/15/2005

Bernard Connolly

067074-0310832

4630

27496 7590 08/20/2009
PILLSBURY WINTHROP SHAW PITTMAN LLP
P.O BOX 10500
McLean, VA 22102

EXAMINER

HUTSON, RICHARD G

ART UNIT

PAPER NUMBER

1652

MAIL DATE

DELIVERY MODE

08/20/2009

PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

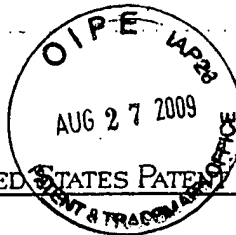
The time period for reply, if any, is set in the attached communication.

RECEIVED

PILLSBURY WINTHROP SHAW PITTMAN

AUG 21 2009

CL _____ MT# _____
ATTY(S) _____
DUE: _____
DKT BY(1) _____ (2) _____



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WASHINGTON, DC 20231
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APPLICATION NO. / CONTROL NO. 10511130	FILING DATE 8/15/2005	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION CONNOLLY ET AL.	ATTORNEY DOCKET NO. 067074-0310832
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EXAMINER
Richard G. Hutson

ART UNIT 1652	PAPER 20090817
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DATE MAILED: 8/17/2009

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents.

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

The addresses below are effective 5 June 2004. Please direct all replies to the United States Patent and Trademark Office via one (1) of the following:

1. Electronically submitted through EFS-Web (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)
2. Mailed to:
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Commissioner for Patents
P.O. Box 22313 1450
Alexandria, VA 22313 1450
3. Hand Carry, Federal Express, United Parcel Service or other delivery service to:
U.S. Patent and Trademark Office
Mail Stop Sequence
Customer Window
Randolph Building
401 Dulany Street
Alexandria, VA 22314

Any inquiry concerning this communication should be directed to Richard Hutson at telephone number 571-272-0930. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Andrew Wang, can be reached on 571-272-0811

/Richard G Hutson/
Primary Examiner, Art Unit 1652



Notice to Comply

Application No.
10511130

Applicant(s)
CONNOLLY ET AL.

Examiner
Richard G. Hutson

Art Unit
1652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment specifically directing its entry into the application.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-0731 or (571) 272-0951

For CRF Submission Help, call (571) 272-2510

PatentIn Software Program Support

Technical Assistance 1-866-217-9197 or 703-305-3028 or 571-272-6845

PatentIn Software is Available At www.USPTO.gov

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

/Richard G Hutson/
Primary Examiner, Art Unit 1652

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=22; hr=9; min=26; sec=4; ms=670;]

=====

Reviewer Comments:

<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES

<130> P89103PWO

<140> 10511130

<141> 2005-08-15

<150> PCT/GB2003/001623

<151> 2003-04-15

<160> 32

Numeric identifier <160> must reflect the total number of sequences found in the sequence listing. This file contains 33 SEQ ID numbers, but <160> states there are 32. Please make all necessary changes.

<210> 13

<211> 103

<212> PRT

<213> RB69

* * * * *

Numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." Please make all necessary changes.

<210> 33
<211> 13
<212> PRT
<213> Unknown
<220>
<223> amino acid motif where X can be any amino acid

<400> 33

Glu Xaa Xaa Ile Xaa Phe/Tyr Xaa Xaa Xaa Tyr Xaa Xaa Asp
1 5 10

Numeric identifier <211> must reflect the total number of amino acids in the sequence. <211> states there are 13 amino acids in SEQ ID # 33, but the actual count is 14. Please make all necessary changes.

A sequence cannot contain any non-sequence related symbols. Please remove "/" from SEQ ID # 33.

Application No: 10511130

Version No: 2.0



Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144

Finished: 2008-09-20 06:22:44.841

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms

Total Warnings: 23

Total Errors: 2

No. of SeqIDs Defined: 32

Actual SeqID Count: 33

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
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W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)

Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144
Finished: 2008-09-20 06:22:44.841
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms
Total Warnings: 23
Total Errors: 2
No. of SeqIDs Defined: 32
Actual SeqID Count: 33

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (33)
E 330	Invalid protein , found in SEQID(33) POS (6)Invalid
W 333	tabs used in amino acid numbering SEQID (33)
E 252	Calc# of Seq. differs from actual; 32 seqIds defined; count=33

SEQUENCE LISTING



<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES

<130> P89103PWO

<140> 10511130

<141> 2005-08-15

<150> PCT/GB2003/001623

<151> 2003-04-15

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 776

<212> PRT

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<220>

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Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys
35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val
50 55 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro
65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
100 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile
115 120 125

Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu
130 135 140

Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met
145 150 155 160

Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn
165 170 175

Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile
180 185 190

Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val
195 200 205

Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala
210 215 220

Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro
225 230 235 240

Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg
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Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro
260 265 270

Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys
275 280 285

Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu
290 295 300

Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr
305 310 315 320

Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg
325 330 335

Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn
340 345 350

Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val
355 360 365

Ala Pro Asn Lys Pro Ser Glu Glu Tyr Gln Arg Arg Leu Arg Glu
370 375 380

Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu
385 390 395 400

Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile
405 410 415

Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn
420 425 430

Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro
435 440 445

Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys
450 455 460

Ile Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu
465 470 475 480

Leu Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr
485 490 495

Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala
500 505 510

Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys
515 520 525

Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp
530 535 540

Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys
545 550 555 560

Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu
565 570 575

Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr
580 585 590

Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg
595 600 605

Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr
610 615 620

Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu
625 630 635 640

Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu
645 650 655

Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu
660 665 670

His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu
675 680 685

Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile

690

695

700

Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu
705 710 715 720

Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu
725 730 735

Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr
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Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr
755 760 765

Ser Trp Leu Asn Ile Lys Lys Ser
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<212> PRT

<213> *Pyrococcus furiosus*

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Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
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Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
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Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370 375 380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
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His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
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Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
435 440 445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
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Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
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Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
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Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
515 520 525

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530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625 630 635 640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
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Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
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Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
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Trp Leu Asn Ile Lys Lys Ser

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<223> Variant derived from *Pyrococcus furiosus* Pfu-Polymerase

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35 40 45

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Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro
65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
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Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile
115 120 125

Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu
130 135 140

Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met
145 150 155 160

Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn
165 170 175

Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile
180 185 190

Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val
195 200 205

Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala
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Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg
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Gly Phe Ile Pro Ser Leu Leu Gly His Leu L